

Figure 1

Primer R
↓ ↓ ↓ ↓ ↓

Target Sequence

PCR amplify
↓
Fok I/F_{sp} I

Digest with Fok I and Fsp I

Seq ID	Seq
CTTGCCCCCAGAAATGATGC	GCATGTCT GTATTACTGGGCGAGGTGTCTCT (Seq ID NO:4)
GAACGGGGGTCTTACCTCT	CCCACAGACATA ATGACCCCGCTCCACAGGA (Seq ID NO:5)

12 mer

Fi

Fok I site

[illegible]

Cut with Fok I

nnnnnGGATGnnnnnnnnnn	nnnnnnnnnnnn
nnnnnCCGACnnnnnnnnnnnn	nnnnnnnn

Fsp I

nnnnnnTGC[↓]GCAnnnnnn
nnnnnnnACGCGTnnnnnn

Cut with Fsp I

nnnnnnTGC	GCAnnnnnn
nnnnnnACG	CGTnnnnn

The diagram is a circle with 'Firm' at the center. Surrounding it are several boxes and labels: 'Market' (top), 'Government' (top-right), 'Industry' (right), 'Society' (bottom-right), 'Environment' (bottom), 'Technology' (bottom-left), 'Economy' (left), and 'Culture' (top-left). Arrows point from each of these outer boxes toward the central 'Firm' box.

Fok I/Fsp I



Figure 6. Introduction of Fok I and Pvu II sites during PCR by loop followed by endonuclease digestion

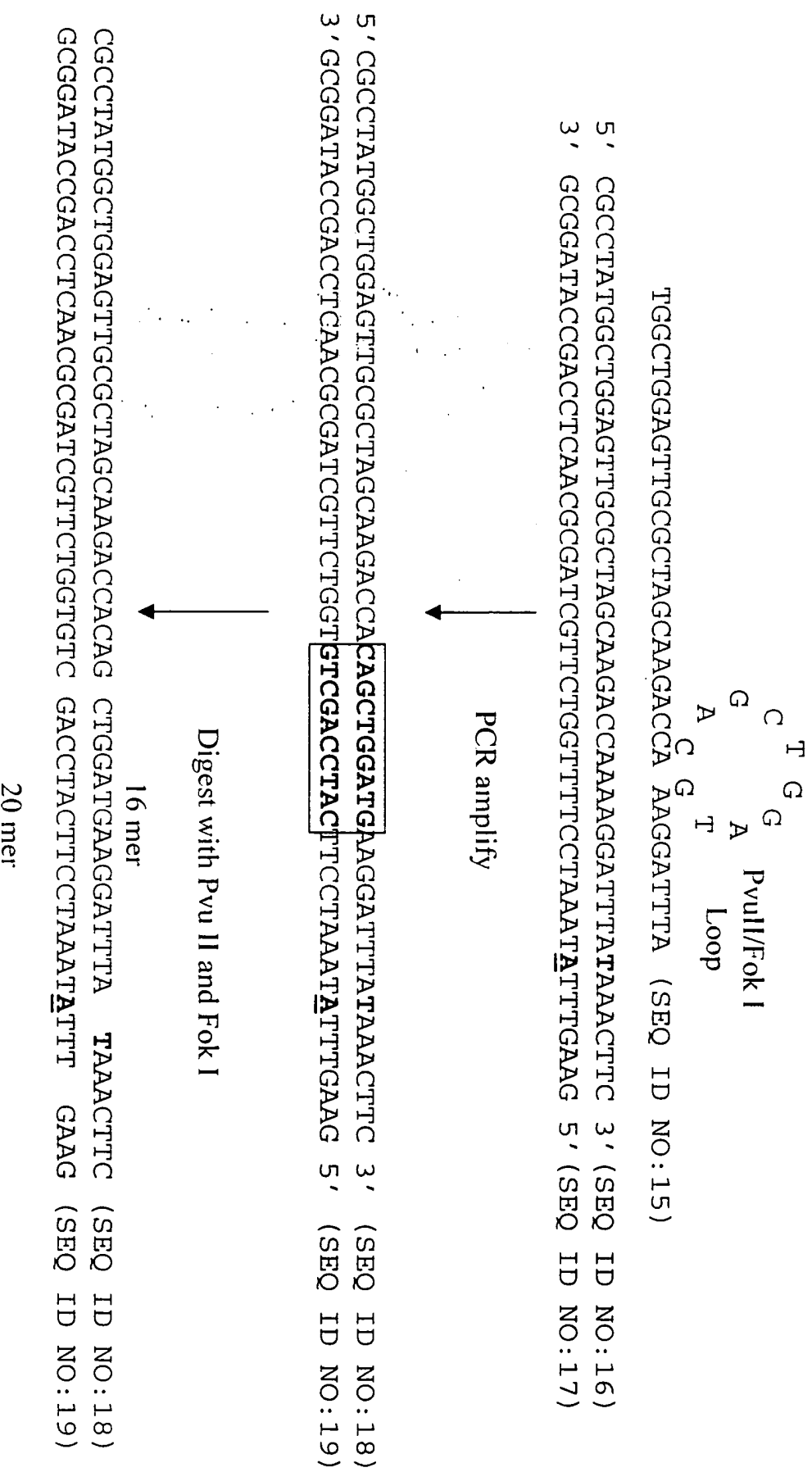


Figure 7

Fok I/Fsp I

CTTGCCCCCAGAAATGGAGGAGGATGGATGGCA GGTGTCTGTATTACTGGCGAGGT (SEQ ID NO:20)
GAACGGGGTCTTACCTCCTCCTACGGCCTCCACAGACA TAATGACCCGCTCCA (SEQ ID NO:21)

↓
Remove nucleotides and
digest with Fok I

CTTGCCCCCAGAAATGGAGGAGGATGCCAGGTGT (SEQ ID NO:22)
GAACGGGGTCTTACCTCCTCCTACGGCTCCACAGACA (SEQ ID NO:23)

↓
Fill in with mass
Modified nucleotide

CTTGCCCCCAGAAATGGAGGAGGATGCCAGGTGTCTGT^{mod} (SEQ ID NO:24)
GAACGGGGTCTTACCTCCTCCTACGGCTCCACAGACA (SEQ ID NO:23)



Ten

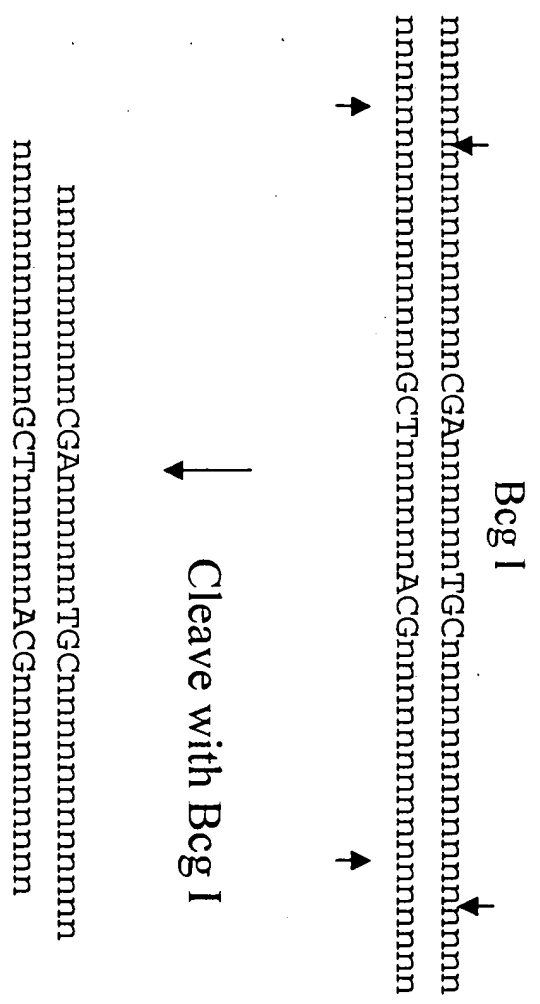


Figure 9

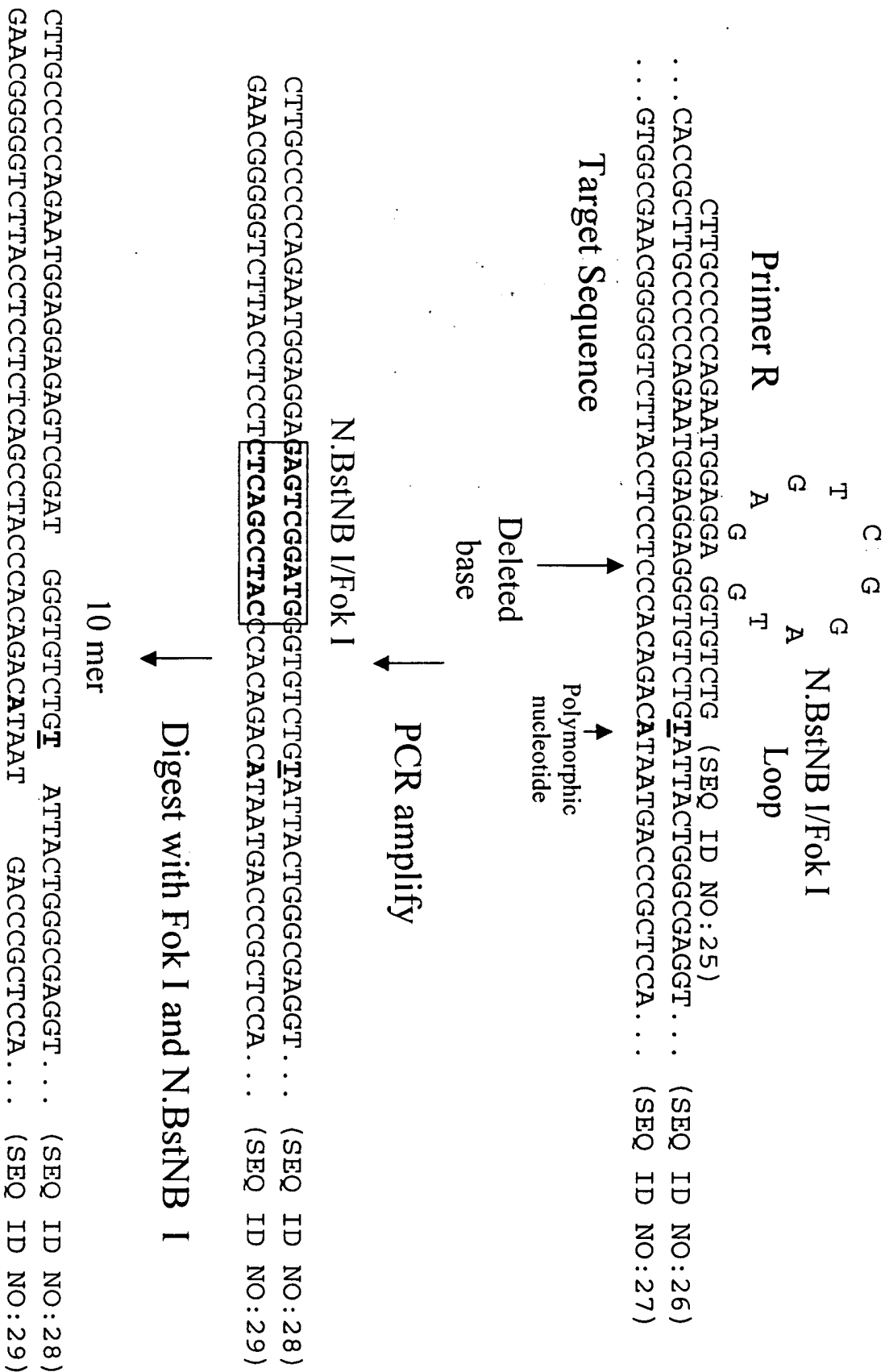


Figure 10

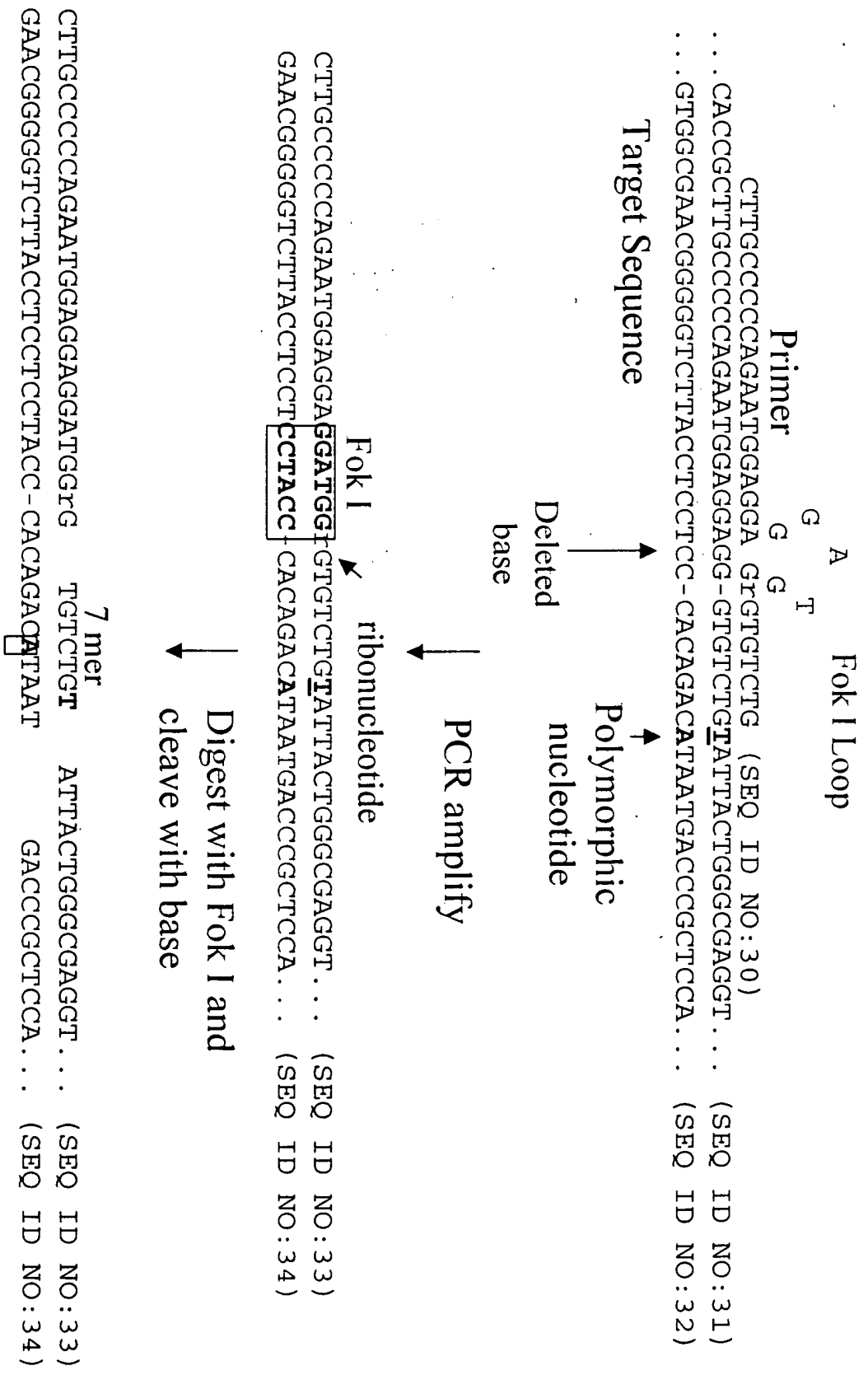


Figure 11. Methods for haplotyping based on physical allele separation

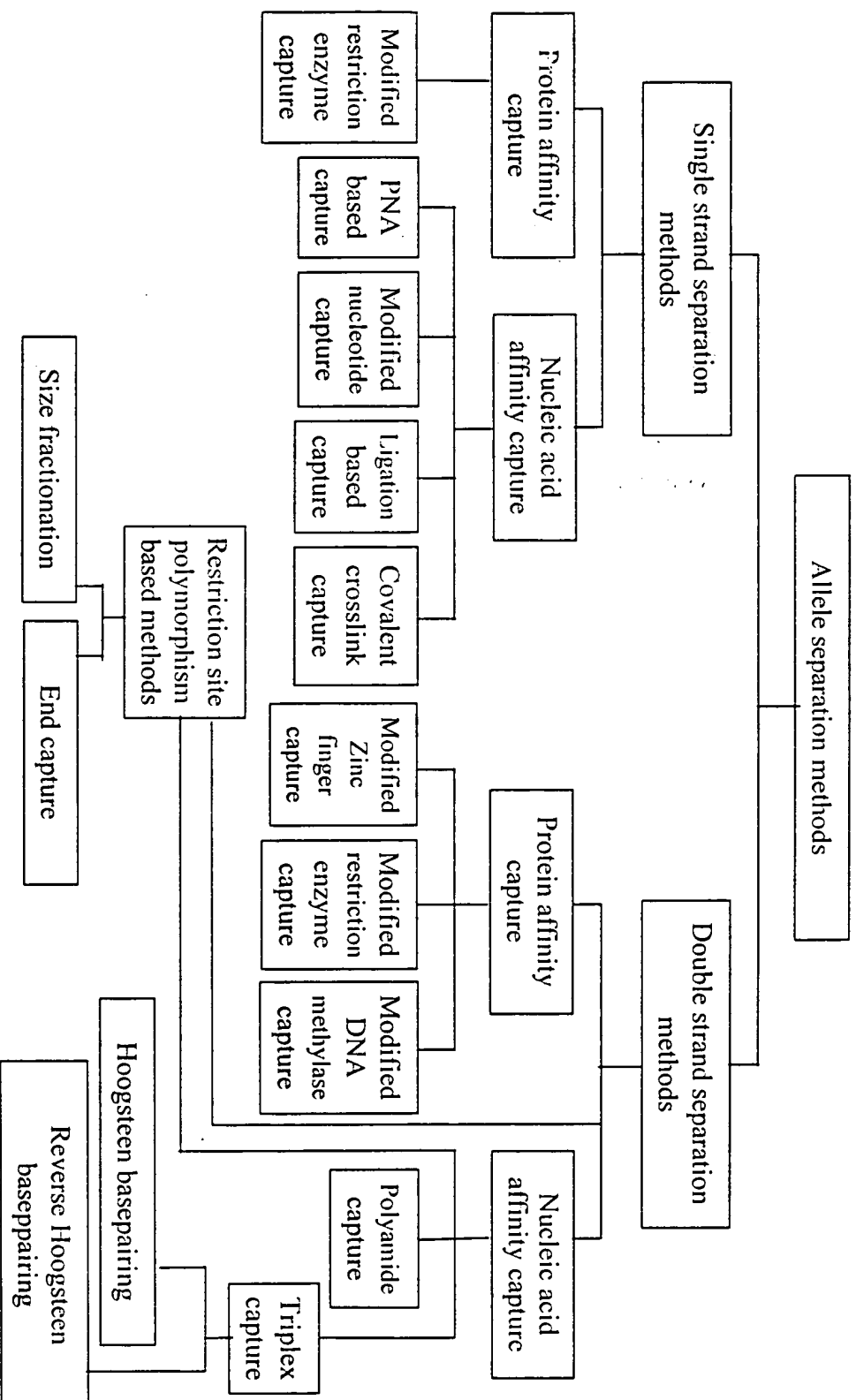
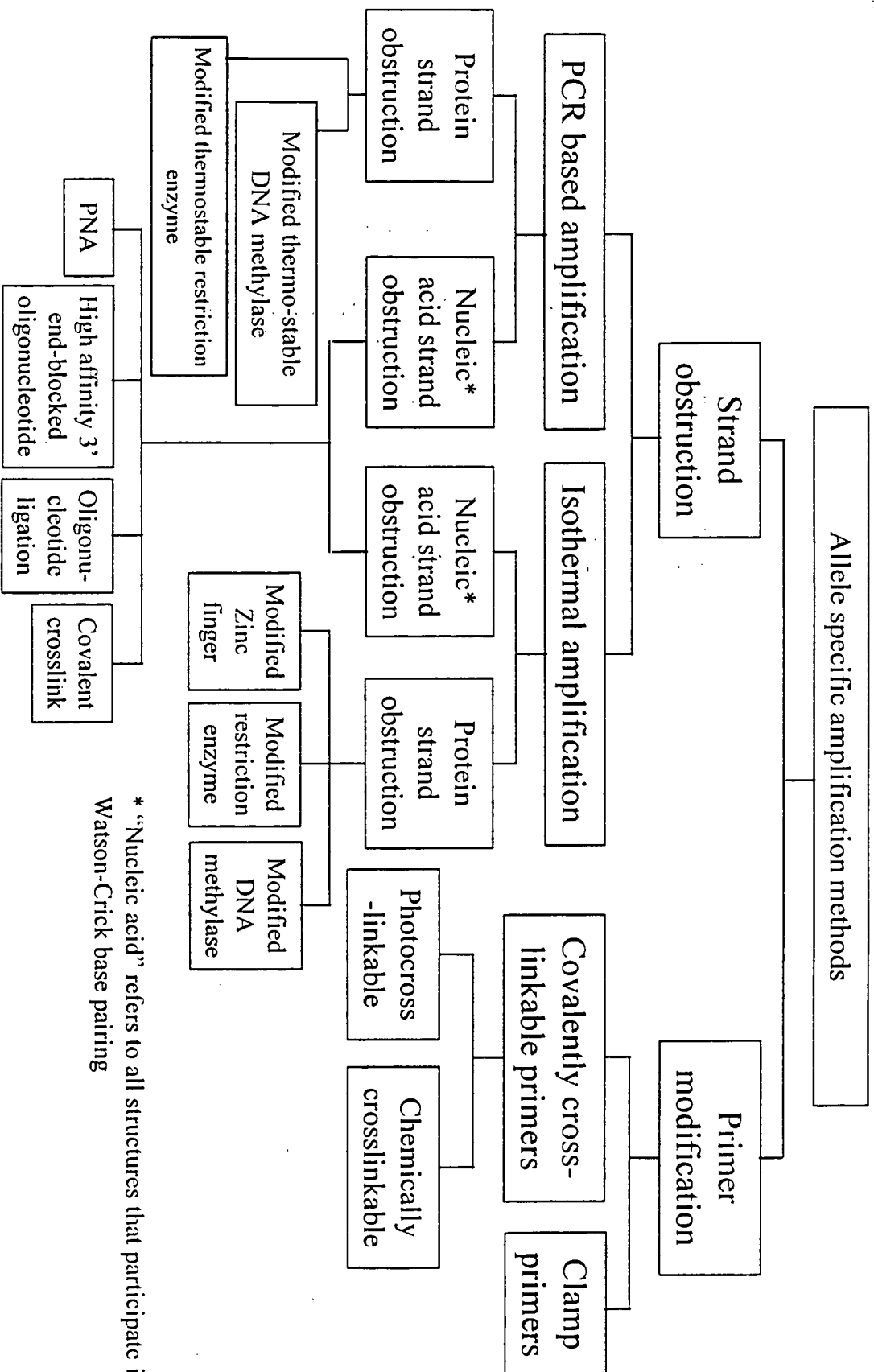


Figure 12. Methods for haplotyping based on allele specific amplification



* "Nucleic acid" refers to all structures that participate in Watson-Crick base pairing

Figure 13. Methods for haplotyping based on allele specific restriction

